

## SEQUENCE LISTING

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&lt;212&gt; DNA

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<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 16

Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg  
1 5 10 15

<210> 17  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 17

Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 1 5 10

<210> 18  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser  
 1 5 10 15

<210> 19  
 <211> 3105  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct

<400> 19

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atgaaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa      60
caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca      120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc      180
gagctccagg cagccccgcg ctgcttcgcc ctgctgtggg gctgtgcgct ggccgcggcc      240
gcggcgggcg agggcaagga agtggtactg ctggactttg ctgcagctgg aggggagctc      300
ggctggctca cacacccgta tggcaaaggg tgggacctga tgcagaacat catgaatgac      360
atgccgatct acatgtactc cgtgtgcaac gtgatgtctg gcgaccagga caactggctc      420
cgcaccaact ggggtgtacc aggagaggct gagcgtatct tcattgagct caagtttact      480
gtacgtgact gcaacagctt ccctgggtgg gccagctcct gcaaggagac tttcaacctc      540
tactatgccg agtcggacct ggactacggc accaacttcc agaagcgcct gttcaccaag      600
attgacacca ttgcgcccga tgagatcacc gtcagcagcg acttcgagga acgccacgtg      660
aagctgaacg tggaggagcg ctccgtgggg ccgctcaccc gcaaaggctt ctacctggcc      720
ttccaggata tccgtgcctg tgtggcgctg ctctccgtcc gtgtctacta caagaagtgc      780
cccagctgc tgcagggcct ggcccacttc cctgagacca tcgccggctc tgatgcacct      840
tccctggcca ctgtggccgg cacctgtgtg gaccatgccg tgggtgccacc gggggggtgaa      900

gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccattgg gcagtgcctg      960
tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggatttttt      1020
aagtttgagg catctgagag cccctgcttg gagtgccttg agcacacgct gccatcccct      1080

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gaggggtgcc	cctcctgcga	gtgtgaggaa	ggcttcttcc	gggcacctca	ggacccagcg	1140
tcgatgcctt	gcacacgacc	cccctccgcc	ccacactacc	tcacagccgt	gggcatgggt	1200
gccaaaggtg	agctgcgctg	gacgccccct	caggacagcg	ggggccgcga	ggacattgtc	1260
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aggaagaacc	agcgtgcccc	ccagtccccg	gaggacgttt	acttctccaa	gtcagaacaa	1920
ctgaagcccc	tgaagacata	cgtggacccc	cacacatatg	aggaccccaa	ccaggctgtg	1980
ttgaagttca	ctaccgagat	ccatccatcc	tgtgtcactc	ggcagaaggt	gatcggagca	2040
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ccggtggcca	tcaagacgct	gaaagccggc	tacacagaga	agcagcgagt	ggacttcctc	2160
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aagtctcttc	gggagaagga	tggcgagttc	agcgtgctgc	agctggtggg	catgctgcgg	2340
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acggagcact tcatggcggc cggctacact gccatcgaga aggtggtgca gatgaccaac 3000  
gacgacatca agaggattgg ggtgcggctg cccggccacc agaagcgcat cgcctacagc 3060  
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<210> 20

<211> 1035

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Leu Gln Ala  
50 55 60

Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala  
65 70 75 80

Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala  
85 90 95

Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp  
100 105 110

Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val  
115 120 125

Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp  
130 135 140

Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr  
145 150 155 160

Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu  
165 170 175

Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn  
 180 185 190

Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu  
 195 200 205

Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val  
 210 215 220

Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala  
 225 230 235 240

Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr  
 245 250 255

Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu  
 260 265 270

Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr  
 275 280 285

Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met  
 290 295 300

His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu  
 305 310 315 320

Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser  
 325 330 335

Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys  
 340 345 350

Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys  
 355 360 365

Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys  
 370 375 380

Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly  
 385 390 395 400

Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg  
 405 410 415



Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser  
 420 425 430

Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro  
 435 440 445

His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His  
 450 455 460

Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu  
 465 470 475 480

Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr  
 485 490 495

Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser  
 500 505 510

Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr  
 515 520 525

Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg  
 530 535 540

Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr  
 545 550 555 560

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala  
 565 570 575

Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly  
 580 585 590

Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu  
 595 600 605

Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln  
 610 615 620

Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln  
 625 630 635 640

Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro  
 645 650 655

Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val  
 660 665 670

Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys  
 675 680 685

Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile  
 690 695 700

Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu  
 705 710 715 720

Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg  
 725 730 735

Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu  
 740 745 750

Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly  
 755 760 765

Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala  
 770 775 780

Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala  
 785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp  
 805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr  
 820 825 830

Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile  
 835 840 845

Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile  
 850 855 860

Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu  
 865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro  
 885 890 895

Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys

900 905 910  
 Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser  
 915 920 925  
 Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala  
 930 935 940  
 Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser  
 945 950 955 960  
 Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys  
 965 970 975  
 Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile  
 980 985 990  
 Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val  
 995 1000 1005  
 Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly  
 1010 1015 1020  
 Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 1025 1030 1035

<210> 21  
 <211> 1506  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgac 120  
 tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac 180  
 tgggtgtacc gaggagagggc tgagcgtatc ttcattgagc tcaagtttac tgtacgtgac 240  
 tgcaacagct tccctgggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc 300  
 gagtcggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc 360  
 attgcgcccc atgagatcac cgtcagcagc gacttcgagg cagccacgt gaagctgaac 420  
 gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat 480  
 atcggtgctt gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg 540  
 ctgcagggcc tggcccactt ccctgagacc atcgccggct ctgatgcacc ttccctggcc 600

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actgtggccg gcacctgtgt ggaccatgcc gtggtgccac cggggggtga agagccccgt    660
atgcactgtg cagtggatgg cgagtggctg gtgcccattg ggcagtgcct gtgccaggca    720
ggctacgaga aggtggagga tgcctgccag gcctgctcgc ctggattttt taagtttgag    780
gcatctgaga gcccctgctt ggagtgccct gagcacacgc tgccatcccc tgaggggtgcc    840
acctcctgcg agtgtgagga aggtttcttc cgggcacctc aggaccacgc gtcgatgcct    900
tgcacacgac cccctccgc cccacactac ctcacagccg tgggcatggg tgccaagggtg    960
gagctgcgct ggacgcccc tcaggacagc gggggccgag aggacattgt ctacagcgtc   1020
acctgcgaac agtgcctggc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc   1080
tactcggagc ctcttcacgg actgaccgc accagtgtga cagtgagcga cctggagccc   1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc   1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg   1260
gagggccgca gcaccacctc gcttagcgtc tcctggagca tccccccgcc gcagcagagc   1320
cgagtgtgga agtacgaggt cacttacgc aagaaggag actccaacag ctacaatgtg   1380
cgccgcaccg agggtttctc cgtgaccctg gacgacctgg cccagacac cacctacctg   1440
gtccaggtgc aggcactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc   1500
cagacg                                           1506

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<210> 22

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human sequence optimized for codon usage in *Listeria*

<400> 22

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caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta    60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaaatt   120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattggtt acgtacaaat   180
tgggtttatc gtggtgaagc agaacgtatt ttatttgaat taaaatttac agttcgtgat   240
tgtaatatgt ttccagggtg tgcaagtagt tgtaaagaaa catttaattt atattatgca   300
gaaagtgatt tagattatgg tacaaatttt caaaaacgtt tatttacaaa aattgataca   360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat   420
gttgaagaac gtagtgttgg tccattaaca cgtaaagggt ttatttttagc atttcaagat   480
attggtgcat gtgttgcat attaatgtgt cgtgtttatt ataaaaaatg tccagaatta   540

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ttacaagggt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca    600
acagttgcag gtacatgtgt tgatcatgca gttgttccac cagggtggtga agaaccacgt    660
atgcattgtg cagttgatgg tgaatgggta gttccaattg gtcaatgttt atgtcaagca    720
ggttatgaaa aagttgaaga tgcattgtcaa gcatgtagtc cagggtttttt taaatttgaa    780
gcaagtgaaa gtccatgttt agaattgtcca gaacatacat taccaagtcc agaagggtgca    840
acaagttgtg aatgtgaaga aggttttttt cgtgcaccac aagatccagc aagtatgccca    900
tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt    960
gaattacgtt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt   1020
acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt   1080
tatagtgaac caccacatgg ttttaacacgt acaagtgtta cagttagtga tttagaacca   1140
catatgaatt atacatttac agttgaagca cgtaatgggt ttagtgggtt agttacaagt   1200
cgtagttttc gtacagcaag tgttagtatt aatcaaacag aaccaccaaa agttcgttta   1260

gaaggtcgta gtacaacaag ttttaagtgt agttggagta ttccaccacc acaacaaagt   1320
cgtgttttga aatatgaagt tacatatcgt aaaaaagggt atagtaatag ttataatgtt   1380
cgtcgtacag aagggttttag tgttacatta gatgatttag caccagatac aacatattta   1440
gttcaagttc aagcattaac acaagaaggt caagggtgcag gtagtcgtgt tcatgaattt   1500
caaaca                                           1506

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<210> 23  
 <211> 502  
 <212> PRT  
 <213> Homo sapeins

<400> 23

Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu  
 1 5 10 15

Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln  
 20 25 30

Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val  
 35 40 45

Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg  
 50 55 60

Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp

65	70	75	80
Cys Asn Ser Phe	Pro Gly Gly Ala	Ser Ser Cys Lys	Glu Thr Phe Asn
	85	90	95
Leu Tyr Tyr Ala	Glu Ser Asp Leu	Asp Tyr Gly Thr	Asn Phe Gln Lys
	100	105	110
Arg Leu Phe Thr	Lys Ile Asp Thr	Ile Ala Pro Asp	Glu Ile Thr Val
	115	120	125
Ser Ser Asp Phe	Glu Ala Arg His	Val Lys Leu Asn	Val Glu Glu Arg
	130	135	140
Ser Val Gly Pro	Leu Thr Arg Lys	Gly Phe Tyr Leu	Ala Phe Gln Asp
	145	150	155
Ile Gly Ala Cys	Val Ala Leu Leu	Ser Val Arg Val	Tyr Tyr Lys Lys
	165	170	175
Cys Pro Glu Leu	Leu Gln Gly Leu	Ala His Phe Pro	Glu Thr Ile Ala
	180	185	190
Gly Ser Asp Ala	Pro Ser Leu Ala	Thr Val Ala Gly	Thr Cys Val Asp
	195	200	205
His Ala Val Val	Pro Pro Gly Gly	Glu Glu Pro Arg	Met His Cys Ala
	210	215	220
Val Asp Gly Glu	Trp Leu Val Pro	Ile Gly Gln Cys	Leu Cys Gln Ala
	225	230	235
Gly Tyr Glu Lys	Val Glu Asp Ala	Cys Gln Ala Cys	Ser Pro Gly Phe
	245	250	255
Phe Lys Phe Glu	Ala Ser Glu Ser	Pro Cys Leu Glu	Cys Pro Glu His
	260	265	270
Thr Leu Pro Ser	Pro Glu Gly Ala	Thr Ser Cys Glu	Cys Glu Glu Gly
	275	280	285
Phe Phe Arg Ala	Pro Gln Asp Pro	Ala Ser Met Pro	Cys Thr Arg Pro
	290	295	300
Pro Ser Ala Pro	His Tyr Leu Thr	Ala Val Gly Met	Gly Ala Lys Val
	305	310	315
			320

Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile  
                                   325                                  330                                  335

Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys  
                                   340                                  345                                  350

Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu  
                                   355                                  360                                  365

Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr  
                                   370                                  375                                  380

Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser  
                                   385                                  390                                  395                                  400

Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro  
                                   405                                  410                                  415

Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp  
                                   420                                  425                                  430

Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr  
                                   435                                  440                                  445

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu  
                                   450                                  455                                  460

Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu  
                                   465                                  470                                  475                                  480

Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg  
                                   485                                  490                                  495

Val His Glu Phe Gln Thr  
                                   500

<210> 24  
 <211> 1689  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 24  
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

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caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
gagcagggca aggaagtggc actgctggac tttgctgcag ctggagggga gctcggctgg 240
ctcacacacc cgtatggcaa aggggtggac ctgatgcaga acatcatgaa tgacatgccg 300
atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360
aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420
gactgcaaca gcttccttgg tggcgccagc tectgcaagg agactttcaa cctctactat 480
gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540
accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600
aacgtggagg agcgctccgt ggggccgctc acccgcaaag gcttctacct ggcttccag 660
gatatcggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720
ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttcctt 780
gccactgtgg ccggcacctg tgtggacat gccgtggtgc caccgggggg tgaagagccc 840
cgtatgcact gtgcagtgga tggcgagtgg ctggtgcccc ttgggcagtg cctgtgccag 900
gcaggctacg agaaggtgga ggatgcctgc caggcctgct cgcttgatt ttttaagttt 960
gaggcatctg agagcccctg cttggagtgc cctgagcaca cgctgccatc ccctgaggg 1020
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ccttgcacac gacccccctc cgccccacac tacctcacag ccgtgggcat gggtgccaag 1140
gtggagctgc gctggacgcc ccctcaggac agcggggggc gcgaggacat tgtctacagc 1200
gtcacctgcg aacagtgcct gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagtgag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagcccc caaggtgagg 1440
ctggagggcc gcagcaccac ctgccttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactcaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctgggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg 1689

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&lt;210&gt; 25

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 25

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys  
 50 55 60

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp  
 65 70 75 80

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met  
 85 90 95

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 100 105 110

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala  
 115 120 125

Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser  
 130 135 140

Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr  
 145 150 155 160

Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe  
 165 170 175

Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp  
 180 185 190

Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly  
 195 200 205

Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala  
 210 215 220

Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu  
 225 230 235 240

Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp  
 245 250 255

Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val  
 260 265 270

Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly  
 275 280 285

Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu  
 290 295 300

Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe  
 305 310 315 320

Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro  
 325 330 335

Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg  
 340 345 350

Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala  
 355 360 365

Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg  
 370 375 380

Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser  
 385 390 395 400

Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys  
 405 410 415

Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr  
 420 425 430

Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr  
 435 440 445

Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe  
 450 455 460

Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg  
465 470 475 480

Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro  
485 490 495

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys  
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser  
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val  
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu  
545 550 555 560

Phe Gln Thr

<210> 26

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 26

```

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac      60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata      120
at attgcgtt tcattcttag aagcgaattt cgccaatatt ataattatca aaagagaggg      180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg      240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa      300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca      360
ccagcatctc cgcttgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc      420
gattataaag atgatgatga taaacaagggt aaagaagttg ttttattaga ttttgcagca      480

gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa      540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtgggtgat      600
caagataatt ggttacgtac aaattggggt tatcgtgggtg aagcagaacg tattttttatt      660

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gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900
ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtgtt 960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttgtt 1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tggatgaatgt 1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaaggt cgtagtaca caagtttaag tgtaggtgg 1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtgttac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagg 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc 1989

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&lt;210&gt; 27

&lt;211&gt; 581

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 27

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala  
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly  
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr  
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr  
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys  
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys  
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly  
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro  
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu  
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr  
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg  
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe  
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala  
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro  
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln  
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala  
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu  
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys  
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met  
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly  
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly  
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro  
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu  
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu  
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser  
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn  
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser  
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp

	500		505		510
Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn					
	515		520		525
Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro					
	530		535		540
Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln					
	545		550		555
Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile					
		565		570	575
Ser Glu Glu Asp Leu					
	580				

<210> 28  
 <211> 1989  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaaacg gtatttggca ttattagggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 aaaaaaatta tgtagtttt tattacatta attttagtta gttaccaat tgcacaacaa 300  
 acagaagcaa aagatgcaag tgcatttaaat aaagaaaata gtattagtag tatggcacca 360  
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420  
 gattataaag atgatgatga taaacaagggt aaagaagttg ttttattaga ttttgcagca 480  
 gcaggtggtg aattagggtg gttaacacat ccatatggta aagggtggga tttaatgcaa 540  
 aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtgggtgat 600  
 caagataatt gggtacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt 660  
 gaattaaaat ttacagttcg tgattgtaat agttttccag gtgggtgcaag tagttgtaaa 720  
 gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780  
 cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840  
 gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900

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ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtggt      960
tattataaaa aatgtccaga attattacaa ggttttagcac attttccaga aacaattgca    1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttggt    1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca    1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt    1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat    1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca    1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca    1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtggt    1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt    1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt    1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat    1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa    1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtaggttgg    1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa    1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtgttac attagatgat    1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaaggt    1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta    1980
tgagagctc                                     1989

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<210> 29
<211> 581
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Predicted Fusion protein

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<400> 29

```

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

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Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30

```

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35          40          45

```



Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala  
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly  
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr  
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr  
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys  
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys  
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly  
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro  
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu  
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr  
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg  
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe  
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala  
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro  
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln  
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala  
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu  
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys  
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met  
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly  
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly  
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro  
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu  
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu  
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser  
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn  
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser  
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp  
 500 505 510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn  
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro  
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln  
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile  
 565 570 575

Ser Glu Glu Asp Leu  
 580

<210> 30  
 <211> 1968  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 30  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcattctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300  
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360  
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420  
 aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attaggttgg 480  
 ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca 540  
 atttatatgt atagtgtttg taatgttatg agtggtgatc aagataattg gttacgtaca 600  
 aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt 660  
 gattgtaata gttttccagg tgggtgcaagt agttgtaaag aaacatttaa tttatattat 720  
 gcagaaagtg atttagatta tgggtacaaat tttcaaaaac gtttatttac aaaaattgat 780  
 acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tgttaaatta 840  
 aatgttgaag aacgtagtgt tgggtccatta acacgtaaag gtttttattt agcatttcaa 900  
 gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa 960  
 ttattacaag gtttagcaca ttttccagaa acaattgcag gtagtgatgc accaagttta 1020  
 gcaacagttg caggtacatg tgttgatcat gcagttgttc caccaggtgg tgaagaacca 1080

```

cgtatgcatt gtgcagttga tggatgaatgg ttagttccaa ttggatcaatg tttatgtcaa 1140
gcagggttatg aaaaagttga agatgcatgt caagcatgta gtccagggtt ttttaaattt 1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt 1260
gcaacaagtt gtgaatgtga agaagggttt tttcgtgcac cacaagatcc agcaagtatg 1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat ggggtcaaaa 1380
gttgaattac gttggacacc accacaagat agtgggtggtc gtgaagatat tgtttatagt 1440
gttacatgtg aacaatgttg gccagaaaagt ggtgaatgtg gtccatgtga agcaagtgtt 1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa 1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgttagtgg tttagttaca 1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt 1680
ttagaagggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa 1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat 1800
gttcgtcgta cagaagggtt tagtgttaca ttagatgatt tagcaccaga tacaacatat 1860
ttagttcaag ttcaagcatt aacacaagaa ggtcaagggtg caggtagtcg tgttcatgaa 1920
tttcaaacag aacaaaaaatt aattagttaa gaagatttat gagagctc 1968

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&lt;210&gt; 31

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted Fusion Protein

&lt;400&gt; 31

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10          15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
          20          25          30

```

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
          35          40          45

```

```

Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gln Gly
          50          55          60

```

```

Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly
        65          70          75          80

```

Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile  
85 90 95

Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser  
100 105 110

Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu  
115 120 125

Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn  
130 135 140

Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr  
145 150 155 160

Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu  
165 170 175

Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser  
180 185 190

Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val  
195 200 205

Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly  
210 215 220

Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro  
225 230 235 240

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser  
245 250 255

Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala  
260 265 270

Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp  
275 280 285

Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr  
290 295 300

Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys  
305 310 315 320

Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu  
                             325                            330                            335

Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe  
                             340                            345                            350

Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser  
                             355                            360                            365

Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu  
                             370                            375                            380

Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr  
                             385                            390                            395                            400

Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro  
                             405                            410                            415

Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg  
                             420                            425                            430

Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe  
                             435                            440                            445

Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser  
                             450                            455                            460

Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val  
                             465                            470                            475                            480

Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile  
                             485                            490                            495

Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg  
                             500                            505                            510

Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe  
                             515                            520                            525

Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln  
                             530                            535                            540

Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His  
                             545                            550                            555                            560

Glu Phe Gln Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

565

570

<210> 32  
 <211> 1254  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgc aggacgttta cttctccaag 60  
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggaccccaac 120  
 caggctgtgt tgaagtccac taccgagatc catccatect gtgtcactcg gcagaagggtg 180  
 atcggagcag gagagtttgg ggaggtgtac aagggcatgc tgaagacatc ctcggggaag 240  
 aaggaggtgc cggtagccat caagacgctg aaagccggct acacagagaa gcagcgagtgc 300  
 gacttcctcg gcgaggccgc catcatgggc cagttcagcc accacaacat catccgccta 360  
 gaggggcgtca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420  
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctggtagggc 480  
 atgctgcggg gcacgcagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540  
 gacctggctg cccgcaacat ctcgtcaac agcaacctgg tctgcaaggt gtctgacttt 600  
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660  
 atccccatcc gctggaccgc cccggaggcc atttccctacc ggaagttcac ctctgccagc 720  
 gacgtgtgga gctttggcat tgtcatgtgg gaggtgatga cctatggcga gcggccctac 780  
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttcgc gctccccaca 840  
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900  
 gcccgccgc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgcccct 960  
 gactccctca agaccctggc tgactttgac ccccgctgt ctatccggct cccagcacg 1020  
 agcggctcgg aggggggtgc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080  
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtgggtgcag 1140  
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200  
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33  
 <211> 1254  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33  
cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa 60  
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaat 120  
caagcagtat taaaatttac aacagaaata cacccaagtt gtgttacaag acaaaaagtt 180  
attggagcag gtgaattcgg agaggtatat aaaggatatgt taaaaacatc atcaggtaaa 240  
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt 300  
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg 360  
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt 420  
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgttttaca attggttggt 480  
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt 540  
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt 600  
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa 660  
attcctattc gttggacagc accagaagct atcagttacc gtaaatttac aagtgcacat 720  
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat 780  
tgggaaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact 840  
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatggtggca acaagaaaga 900  
gcacgacgtc caaaatttgc agatattgtt agtatttttag acaaattaat tcgtgcacca 960  
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg 1020  
tcagggttccg aaggagttcc atttcgcaca gtctccgaat gggtggaatc aattaaatg 1080  
caacaatata ccgaacactt tatggcagca gggtacacag caatcgaaaa agttgttcaa 1140  
atgacaaatg atgatattaa acgtattgga gttagattac caggccacca gaaacgtatt 1200  
gcatattctt tattaggttt aaaagatcaa gttaataccg tgggaattcc aatt 1254

<210> 34  
<211> 456  
<212> PRT  
<213> Homo sapiens

<400> 34

Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala  
1 5 10 15

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala  
20 25 30

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg  
35 40 45



Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro  
 50 55 60

Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala  
 65 70 75 80

Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln  
 85 90 95

Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu  
 100 105 110

Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu  
 115 120 125

Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala  
 130 135 140

Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly  
 145 150 155 160

Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu  
 165 170 175

Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser  
 180 185 190

Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys  
 195 200 205

Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn  
 210 215 220

Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu  
 225 230 235 240

Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly  
 245 250 255

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg  
 260 265 270

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp  
 275 280 285

Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His  
 290 295 300

Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met  
 305 310 315 320

Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln  
 325 330 335

Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp  
 340 345 350

Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp  
 355 360 365

Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val  
 370 375 380

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln  
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val  
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro  
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln  
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile  
 450 455

<210> 35

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

<400> 35

atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120

ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180

gagcaccgca ggaggaagaa ccagcgtgcc cgccagtccc cggaggacgt ttactttctcc 240  
 aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300  
 aaccaggctg tgttgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360  
 gtgatcggag caggagagtt tggggaggtg tacaagggca tgctgaagac atcctcgggg 420  
 aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480  
 gtggacttcc tcggcgagggc cggcatcatg ggccagttca gccaccacaa catcatccgc 540  
 ctagagggcg tcattctcaa atacaagccc atgatgatca tctactgagta catggagaat 600  
 ggggccctgg acaagttcct tcggggagaag gatggcgagt tcagcgtgct gcagctggtg 660  
 ggcattgctgc ggggcattgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720  
 cgtgacctgg ctgcccgcaa catcctcgtc aacagcaacc tggctctgaa ggtgtctgac 780  
 tttggcctgt cccgcgtgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840  
  
 aagatcccca tccgctggac cgccccggag gccatttcct accggaagtt cacctctgcc 900  
 agcgacgtgt ggagctttgg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960  
 tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020  
 acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080  
 cgtgcccgc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140  
 cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200  
 acgagcggct cggagggggg gcccttcgc acggtgtccg agtggctgga gtccatcaag 1260  
 atgcagcagt atacggagca cttcatggcg gccggctaca ctgccatcga gaaggtggtg 1320  
 cagatgacca acgacgacat caagaggatt ggggtgcggc tgcccggcca ccagaagcgc 1380  
 atcgctaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

&lt;210&gt; 36

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted Protein Sequence

&lt;400&gt; 36

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg  
 50 55 60

Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser  
 65 70 75 80

Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr  
 85 90 95

Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His  
 100 105 110

Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly  
 115 120 125

Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val  
 130 135 140

Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg  
 145 150 155 160

Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His  
 165 170 175

Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met  
 180 185 190

Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg  
 195 200 205

Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg  
 210 215 220

Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His  
 225 230 235 240

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys  
 245 250 255

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu  
 260 265 270

Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala  
 275 280 285

Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp  
 290 295 300

Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro  
 305 310 315 320

Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly  
 325 330 335

Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu  
 340 345 350

Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala  
 355 360 365

Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu  
 370 375 380

Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser  
 385 390 395 400

Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu  
 405 410 415

Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly  
 420 425 430

Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys  
 435 440 445

Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser  
 450 455 460

Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 465 470 475

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta ttttctatc ttaaagttac ttttatgtgg aggcattaac	60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca	360
ccagcatctc cgctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagacc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaagg	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacacgc agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggt tggatgtta agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa ataccctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaaactt tagcagactt tgatcctcgt	1440
gtagtatctt gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737

&lt;210&gt; 38

&lt;211&gt; 497

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 38

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln  
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu  
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val  
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys  
 115 120 125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys  
 130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys  
 145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly  
 165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val  
 180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn  
 195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val  
 210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr  
 225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly  
 275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys  
 290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu  
 305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu  
 325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp  
 340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu  
 355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly



450

455

460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
 485 490 495

Leu

&lt;210&gt; 39

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion protein construct

&lt;400&gt; 39

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ggtagctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac      60
atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata      120
atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg      180
gtggcacaacg gtatttggca ttattagggt aaaaaatgta gaaggagagt gaaacccatg      240
aaaaaaatta tgtagttttt tattacatta attttagtta gtttaccaat tgcacaacaa      300
acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca      360
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc      420
gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc      480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat      540
ccgcatacgt acgaagacc aaatcaagca gtattaaaat ttacaacaga aatacaccca      600
agttgtgtta caagacaaaa agttattgga gcagggtgaat tcggagaggt atataaaggt      660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca      720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggccaattt      780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt      840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatgggtgaa      900
tttagtggtt tacaattggg tggtatgtta agaggaattg ctgcagggtat gaaatattta      960
gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat     1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca     1080
acctatacaa catcggggagg taaaattcct attcggttga cagcaccaga agctatcagt     1140

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taccgtaa at ttacaagtgc atcagacgtg tggagttttg ggattgta at gtgggaagtt 1200  
 atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt 1260  
 aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg 1320  
 atgcaatgtt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt 1380  
 ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt 1440  
 gttagtattc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc 1500  
 gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac 1560  
 acagcaatcg aaaaagttgt tcaa atgaca aatgatgata ttaa acgtat tggagttaga 1620  
 ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat 1680  
 accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc 1737

<210> 40

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln  
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu  
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val  
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys

115	120	125
Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys 130 135 140		
Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys 145 150 155 160		
Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly 165 170 175		
Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val 180 185 190		
Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn 195 200 205		
Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val 210 215 220		
Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 225 230 235 240		
Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 245 250 255		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 260 265 270		
Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly 275 280 285		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys 290 295 300		
Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu 305 310 315 320		
Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu 325 330 335		
Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp 340 345 350		
Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu 355 360 365		

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly  
 450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
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Leu

<210> 41  
 <211> 1716  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

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 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300  
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360  
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

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&lt;210&gt; 42

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 42

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Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly

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65					70					75					80															
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225					230					235					240															
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val															
				245				250						255																
Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro															
			260					265					270																	

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 275 280 285

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
 290 295 300

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
 305 310 315 320

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
 325 330 335

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
 340 345 350

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe  
 355 360 365

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser  
 370 375 380

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro  
 385 390 395 400

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp  
 405 410 415

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala  
 420 425 430

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile  
 435 440 445

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr  
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Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
 485 490

<210> 43  
 <211> 9808  
 <212> DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion Protein Construct

&lt;400&gt; 43

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 <211> 26  
 <212> PRT  
 <213> *Listeria monocytogenes*  
 <400> 44

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp  
 20 25

<210> 45  
 <211> 59  
 <212> PRT  
 <213> *Listeria monocytogenes*  
 <400> 45

Met Thr Asp Lys Lys Ser Glu Asn Gln Thr Glu Lys Thr Glu Thr Lys  
 1 5 10 15

Glu Asn Lys Gly Met Thr Arg Arg Glu Met Leu Lys Leu Ser Ala Val  
 20 25 30

Ala Gly Thr Gly Ile Ala Val Gly Ala Thr Gly Leu Gly Thr Ile Leu

35

40

45

Asn Val Val Asp Gln Val Asp Lys Ala Leu Thr  
 50 55

<210> 46  
 <211> 53  
 <212> PRT  
 <213> Bacillus subtilus  
 <400> 46

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu  
 1 5 10 15

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly  
 20 25 30

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser  
 35 40 45

Val Gly Ala Phe Gly  
 50

<210> 47  
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<220>  
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<220>  
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<400> 48  
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<220>  
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<210> 50  
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<220>  
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<210> 51  
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<220>  
<223> Description of Artificial Sequence: Epitope insert

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gattataaaag atgatgatga taaa 24

<210> 52  
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<400> 52

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 53  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 53  
gaacaaaaat taattagtga agaagattta 30

<210> 54  
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<220>

<223> Description of Artificial Sequence: Epitope

<400> 54

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
1 5 10

<210> 55

<211> 9

<212> PRT

<213> Mus sp.

<400> 55

Ser Pro Ser Tyr Val Tyr His Gln Phe  
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 56

Ser Pro Ser Tyr Ala Tyr His Gln Phe  
1 5

<210> 57

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 57

ctctggtacc tcctttgatt agtatattc

29

<210> 58

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 58

caatggatcc ctcgagatca taatttactt catccc

36

<210> 59

<211> 32

<212> DNA



## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 59

atttctcgag tccatggggg gttctcatca tc

32

&lt;210&gt; 60

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 60

ggtgctcgag tgcggccgca agctt

25

&lt;210&gt; 61

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 61

cgattcccct agttatgttt accaccaatt tgctgca

37

&lt;210&gt; 62

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 62

gcaaattggt ggtaaacata actaggggaa t

31

&lt;210&gt; 63

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Epitope insert

&lt;400&gt; 63

agtcgaagtt atgcatatca tcaattt

27

&lt;210&gt; 64

&lt;211&gt; 33

&lt;212&gt; DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 64

cgatagtcga agttatgcat atcatcaatt tgc

33

&lt;210&gt; 65

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 65

gtcgcaaatt gatgatatgc ataacttgga ctat

34

&lt;210&gt; 66

&lt;211&gt; 8

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Consensus Sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1)

&lt;223&gt; n is a, c, g, or u

&lt;400&gt; 66

naggaggu

8

&lt;210&gt; 67

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Listeria monocytogenes

&lt;400&gt; 67

aaggagagt aaacccatg

19

&lt;210&gt; 68

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Listeria monocytogenes

&lt;400&gt; 68

ggtagctcct ttgattagta tttcctatc ttaaagtgac ttttatgttg aggcattaac 60

atattgttaac gacgataaag ggacagcagg actagaataa agctataaag caagcatata 120

atattgcgtt tcattcttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180

gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 69  
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 <212> DNA  
 <213> *Listeria monocytogenes*

<400> 69  
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 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 70  
 <211> 5  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 70

Thr Glu Ala Lys Asp  
 1 5

<210> 71  
 <211> 5  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 71

Asp Lys Ala Leu Thr  
 1 5

<210> 72  
 <211> 5  
 <212> PRT  
 <213> *Bacillus subtilus*

<400> 72

Val Gly Ala Phe Gly  
 1 5